

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT: Gately, Maurice K.  
Presky, David H.

10 (ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Hoffmann-La Roche Inc.  
(B) STREET: 340 Kingsland Street  
(C) CITY: Nutley  
(D) STATE: New Jersey  
(E) COUNTRY: United States  
20 (F) ZIP: 07110-1199

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Buchholz, Briana C.  
(B) REGISTRATION NUMBER: 39,123  
(C) REFERENCE/DOCKET NUMBER: CD 1048P

(ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 973-235-6208  
(B) TELEFAX: 973-235-2363

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: mouse

(G) CELL TYPE: Hybridoma

(H) CELL LINE: HIL-12F3-16G2

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC  
48

Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser  
1 5 10 15

CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC  
96

Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn  
20 25 30

TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA  
144

Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile  
35 40 45

AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC  
192

Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val  
50 55 60

TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT  
240

Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser  
65 70 75 80

TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT TAC TGT GCA AGA TCT TCG  
288

Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser  
85 90 95

GAT GCT TTG GAC TAC TGG GGC GCA GGG ACC ACG  
321

Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser  
1 5 10 15  
Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn  
20 25 30  
Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile  
35 40 45  
Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val  
50 55 60  
Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser  
65 70 75 80  
Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser  
85 90 95  
Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: mouse

(G) CELL TYPE: Hybridoma

(H) CELL LINE: HIL-12F3-20E11

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10 GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC  
48  
Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu  
1 5 10 15

15 ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG  
96  
Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp  
20 25 30

20 ATC CGG AAA TTC CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA AGT  
144  
Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser  
35 40 45

25 TAC AGT GGT AGT ACT TAC TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC  
192  
Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser  
50 55 60

30 ATC ACT CGA GAC ACA TCC AAG AAC CAG TAC TCC ATG CAG TTG AAT TCT  
240  
Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser  
65 70 75 80

35 GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TCC TCG GAT  
288  
Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp  
85 90 95

40 GCT ATG GAC TAC TGG GGC GC  
308  
Ala Met Asp Tyr Trp Gly  
100

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu  
1 5 10 15  
Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp  
20 25 30  
Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser  
35 40 45  
Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser  
50 55 60  
Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser  
65 70 75 80  
Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp  
85 90 95  
Ala Met Asp Tyr Trp Gly  
100